

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/909,2070
Source: 1 Fw/16
Date Processed by STIC: 9/21/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/21/2005

PATENT APPLICATION: US/09/909,207D

TIME: 11:13:43

Input Set : A:\GC450-D1-US-SEQLIST.TXT

Output Set: N:\CRF4\09212005\I909207D.raw

4 <110> APPLICANT: De Buyl, Eric
 5 Lahaye, Andree
 6 Ledoux, Pierre
 7 Detroz, Rene
 9 <120> TITLE OF INVENTION: Xylanase, Microorganisms Producing it,
 10 DNA Molecules, Methods for Preparing this Xylanase and Uses
 11 of the Latter
 13 <130> FILE REFERENCE: GC450-D1-US
 15 <140> CURRENT APPLICATION NUMBER: US 09/909,207D
 16 <141> CURRENT FILING DATE: 2001-07-19
 18 <150> PRIOR APPLICATION NUMBER: US 08/470,953
 19 <151> PRIOR FILING DATE: 1995-06-06
 21 <150> PRIOR APPLICATION NUMBER: BE 09500448
 22 <151> PRIOR FILING DATE: 1995-05-17
 24 <150> PRIOR APPLICATION NUMBER: BE 09400706
 25 <151> PRIOR FILING DATE: 1994-07-26
 27 <160> NUMBER OF SEQ ID NOS: 29
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 663
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Bacillus sp.
 36 <400> SEQUENCE: 1
 37 caaatcg tca cgcacaattc cattggcaac cacgatggct atgattatga attttggaaa 60
 38 gatagcgggtg gctctgggac aatgattctc aatcatggcg gtacgttcag tgcccaatgg 120
 39 aacaatgtta acaacatatt attccgtaaa ggtaaaaaat tcaatgaaac acaaacacac 180
 40 caacaagttg gtaacatgtc cataaactac ggagccaact tccaaccaa tggtaatgcg 240
 41 tattttatgcg tctatggttg gactgttgac cctcttgctg aatattatat tgctcgacagt 300
 42 tgggggcaact ggcgtccacc aggagcaacg cctaagggga ccatcactgt tgatggagga 360
 43 acatatgata tctacgagac tcttagagtc aatcaacct ccattaaggg gattgccaca 420
 44 tttaaacaaat attggagtgt tcgaagatcg aaacgcacga gtggcacgat ttctgtcagc 480
 45 aaccacttta gagcgtggga aaacttaggg atgaatatgg ggaaaatgta tgaagtcgcg 540
 46 cttactgtag aaggctatca aagtagcgga agtgctaag tatatagcaa tacactaaga 600
 47 attaacggta accctctctc aactattagt aatgacgaga gcataacttt ggataaaaac 660
 48 aat 663
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 663
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Bacillus sp.
 55 <220> FEATURE:
 56 <221> NAME/KEY: CDS
 57 <222> LOCATION: (1)...(663)
 59 <221> NAME/KEY: mat_peptide

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60 <222> LOCATION: (1)...(663)
W--> 62 <400> 2
63 caa atc gtc acc gac aat tcc att ggc aac cac gat ggc tat gat tat      48
64 Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr
65 1 5 10 15
67 gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat      96
68 Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His
69 20 25 30
71 ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc      144
72 Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe
73 35 40 45
75 cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt      192
76 Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
77 50 55 60
79 aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg      240
80 Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
81 65 70 75 80
83 tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat      288
84 Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
85 85 90 95
87 att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag      336
88 Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
89 100 105 110
91 ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt      384
92 Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
93 115 120 125
95 aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat      432
96 Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr
97 130 135 140
99 tgg agt gtt cga aga tcg aaa cgc acg agt ggc acg att tct gtc agc      480
100 Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser
101 145 150 155 160
103 aac cac ttt aga gcg tgg gaa aac tta ggg atg aat atg ggg aaa atg      528
104 Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
105 165 170 175
107 tat gaa gtc gcg ctt act gta gaa ggc tat caa agt agc gga agt gct      576
108 Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
109 180 185 190
111 aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act      624
112 Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr
113 195 200 205
115 att agt aat gac gag agc ata act ttg gat aaa aac aat      663
116 Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
117 210 215 220
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 221
122 <212> TYPE: PRT
123 <213> ORGANISM: Bacillus sp.
125 <400> SEQUENCE: 3

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```

126 Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr
127 1 5 10 15
128 Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His
129 20 25 30
130 Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe
131 35 40 45
132 Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
133 50 55 60
134 Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
135 65 70 75 80
136 Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
137 85 90 95
138 Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
139 100 105 110
140 Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
141 115 120 125
142 Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr
143 130 135 140
144 Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser
145 145 150 155 160
146 Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
147 165 170 175
148 Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
149 180 185 190
150 Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr
151 195 200 205
152 Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
153 210 215 220

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155 <210> SEQ ID NO: 4

156 <211> LENGTH: 744

157 <212> TYPE: DNA

158 <213> ORGANISM: Bacillus sp.

160 <400> SEQUENCE: 4

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161 atgagacaaa agaaattgac gttgatttta gccttttttag tttgttttgc actaacctta 60
162 cctgcagaaa taattcaggc acaaatcgtc accgacaatt ccattggcaa ccacgatggc 120
163 tatgattatg aattttggaa agatagcggg ggctctggga caatgattct caatcatggc 180
164 ggtacgttca gtgcccaatg gaacaatgtt aacaacatat tattccgtaa aggtaaaaaa 240
165 ttcaatgaaa cacaaacaca ccaacaagtt ggtaacatgt ccataaacta cggagccaac 300
166 ttccaaccaa atggtaatgc gtatttatgc gtctatgggt ggactgttga ccctcttgtc 360
167 gaatattata ttgtcgacag ttggggcaac tggcgctccac caggagcaac gcctaagggg 420
168 accatcactg ttgatggagg aacatatgat atctacgaga ctcttagagt caatcaaccc 480
169 tccattaagg ggattgccac atttaaacia tattggagtg ttcgaagatc gaaacgcacg 540
170 agtggcacga tttctgtcag caaccacttt agagcgtggg aaaacttagg gatgaatatg 600
171 gggaaaatgt atgaatcgct gcttactgta gaaggctatc aaagtagcgg aagtgctaata 660
172 gtatatagca atacactaag aattaacggg aaccctctct caactattag taatgacgag 720
173 agcataactt tggataaaaa caat 744

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175 <210> SEQ ID NO: 5

176 <211> LENGTH: 744

177 <212> TYPE: DNA

RAW SEQUENCE LISTING

DATE: 09/21/2005

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Input Set : A:\GC450-D1-US-SEQLIST.TXT

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178 <213> ORGANISM: Bacillus sp.
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)...(744)
184 <221> NAME/KEY: mat_peptide
185 <222> LOCATION: (1)...(744)
W--> 187 <221> sig_peptide
188 <222> LOCATION: (82)...(744)
W--> 190 <400> 5
191 atg aga caa aag aaa ttg acg ttg att tta gcc ttt tta gtt tgt ttt      48
192 Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe
193 1 5 10 15
195 gca cta acc tta cct gca gaa ata att cag gca caa atc gtc acc gac      96
196 Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
197 20 25 30
199 aat tcc att ggc aac cac gat ggc tat gat tat gaa ttt tgg aaa gat      144
200 Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
201 35 40 45
203 agc ggt ggc tct ggg aca atg att ctc aat cat ggc ggt acg ttc agt      192
204 Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
205 50 55 60
207 gcc caa tgg aac aat gtt aac aac ata tta ttc cgt aaa ggt aaa aaa      240
208 Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
209 65 70 75 80
211 ttc aat gaa aca caa aca cac caa caa gtt ggt aac atg tcc ata aac      288
212 Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
213 85 90 95
215 tac gga gcc aac ttc caa cca aat ggt aat gcg tat tta tgc gtc tat      336
216 Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr
217 100 105 110
219 ggt tgg act gtt gac cct ctt gtc gaa tat tat att gtc gac agt tgg      384
220 Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
221 115 120 125
223 ggc aac tgg cgt cca cca gga gca acg cct aag ggg acc atc act gtt      432
224 Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
225 130 135 140
227 gat gga gga aca tat gat atc tac gag act ctt aga gtc aat caa ccc      480
228 Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro
229 145 150 155 160
231 tcc att aag ggg att gcc aca ttt aaa caa tat tgg agt gtt cga aga      528
232 Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg
233 165 170 175
235 tcg aaa cgc acg agt ggc acg att tct gtc agc aac cac ttt aga gcg      576
236 Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala
237 180 185 190
239 tgg gaa aac tta ggg atg aat atg ggg aaa atg tat gaa gtc gcg ctt      624
240 Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu
241 195 200 205
243 act gta gaa ggc tat caa agt agc gga agt gct aat gta tat agc aat      672

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RAW SEQUENCE LISTING

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244 Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn
245      210                      215                      220
247 aca cta aga att aac ggt aac cct ctc tca act att agt aat gac gag      720
248 Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu
249 225                      230                      235                      240
251 agc ata act ttg gat aaa aac aat      744
252 Ser Ile Thr Leu Asp Lys Asn Asn
253      245
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 248
258 <212> TYPE: PRT
259 <213> ORGANISM: Bacillus sp.
261 <400> SEQUENCE: 6
262 Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe
263 1      5      10      15
264 Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
265      20      25      30
266 Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
267      35      40      45
268 Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
269      50      55      60
270 Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
271 65      70      75      80
272 Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
273      85      90      95
274 Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr
275      100      105      110
276 Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
277      115      120      125
278 Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
279      130      135      140
280 Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro
281 145      150      155      160
282 Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg
283      165      170      175
284 Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala
285      180      185      190
286 Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu
287      195      200      205
288 Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn
289      210      215      220
290 Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu
291 225      230      235      240
292 Ser Ile Thr Leu Asp Lys Asn Asn
293      245
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 81
297 <212> TYPE: DNA
298 <213> ORGANISM: Bacillus sp.

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/21/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:26; N Pos. 107

VERIFICATION SUMMARY

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Input Set : A:\GC450-D1-US-SEQLIST.TXT

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L:62 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:382 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:385 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:60